Amendments to the Claims:

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

Claims 1-58. (Canceled)

59. (Currently Amended) The construct of claim 79, 80 or 81, wherein the linker moiety comprises between 5 amino acids and 50 amino acids.

60. (Currently Amended) The construct of claim 79, 80 or 81, wherein the donor moiety acceptor moiety and the linker moiety are fused in a single amino acid sequence.

61. (Currently Amended) The construct of claim 79, 80 or 81, wherein the linker comprises a cleavage recognition site for trypsin, enterokinase, HIV -1 protease, prohormone convertase, interleukin-1 b-converting enzyme, adenovirus endopeptidase, cytomegalovirus assemblin, leishmanolysin, b-Secretase for APP, thrombin, renin, angiotensin-converting enzyme, cathepsin D or a kininogenase.

Claims 62-75. (Withdrawn)

76. (Canceled)

77. (Withdrawn)

78. (Withdrawn)

79. (New) A tandem fluorescent protein constrct comprising:

i) a donor fluorescent protein moiety comprising an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Phe64Leu, Ser65Thr, Tyr66Trp, Asn146Ile, Met153Thr, Val163A and Asn212Lys;

b) Ser65Gly, Val68Leu, Ser72Ala and Thr203Tyr;

c) Tyr66His and Tyr145Phe;

d) Tyr66Trp, Asn146Ile, Met153Thr, Val163Ala and Asn212Lys;

e) Ser72Ala, Tyr145Phe and Thr203Ile; and

f) Ser65Thr, Ser72Ala, Asn149Lys, Met153Thr and Ile167Thr;

ii) an acceptor fluorescent protein moiety comprising an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Ser65Gly, Val68Leu, Ser72Ala and Thr203Tyr; and

b) Ser65Thr, Ser72Ala~ Asn149Lys, Met153Thr and Ile167Thr; and

iii) a linker moiety that couples the donor moiety of i) and the acceptor moiety of ii), wherein the linker moiety comprises a protease recognition site.

80. (New) A tandem fluorescent protein construct comprising:

i) a donor fluorescent protein moiety comprising an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Tyr66His and Tyr145Phe; and

b) Tyr66Trp, Asn146Ile, Met153Thr, Val163Ala and Ans212Lys;

ii) an acceptor fluorescent protein moiety comprising an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Ser65Cys; and

b) Ser65Thr; and

iii) a linker moiety that couples the donor moiety of i) and the acceptor moiety of ii), wherein the linker moiety comprises a protease recognition site.

81. (New) A tandem fluorescent protein construct comprising:

A) a donor fluorescent protein moiety comprising:

i) an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Phe64Leu, Ser65Thr, Tyr66Trp, Asn146Ile, Met153Thr, Val163A and Asn212Lys;

b) Ser65Gly, Val68Leu, Ser72Ala and Thr203Tyr;

c) Tyr66His and Tyr145Phe;

d) Tyr66Trp, Asn146Ile, Met153Thr, Val163Ala and Asn212Lys;

e) Ser72Ala, Tyr145Phe and Thr203Ile; and

f) Ser65Thr, Ser72Ala, Asn149Lys, Met153Thr and Ile167Thr; or

ii) an amino acid sequence substantially identical to SEQ ID NO:2 and comprising a mutation that reduces the hydrophobicity at positions A206, L221 or F223, wherein the mutation attenuates the intermolecular interactions between the donor and acceptor moieties;

B) an acceptor fluorescent protein moiety comprising:

i) an amino acid sequence substantially identical to SEQ ID NO:2, and which differs from SEQ ID NO:2 by amino acid substitutions selected from the group consisting of:

a) Ser65Gly, Val68Leu, Ser72Ala and Thr203Tyr; and

b) Ser65Thr, Ser72Ala, Asn149Lys, Met153Thr and Ile167Thr; or

ii) an amino acid sequence substantially identical to SEQ ID NO:2 and comprising a mutation that reduces the hydrophobicity at positions A206, L221 or F223, wherein the mutation attenuates the intermolecular interactions between the donor and acceptor moieties; and

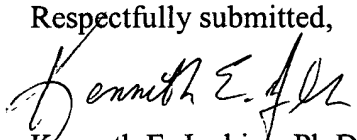
C) a linker moiety that couples the donor moiety of A) and the acceptor moiety of B), wherein the linker moiety comprises a protease recognition site.

CONCLUSION

In view of the foregoing, Applicants believe all claims now pending in this Application are in condition for allowance. The issuance of a formal Notice of Allowance at an early date is respectfully requested.

If the Examiner believes a telephone conference would expedite prosecution of this application, please telephone the undersigned at 858-350-6100.

Respectfully submitted,



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